## Title: Perfect score: Searched: Run on: OM protein - protein search, using sw model Scoring table: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 June 17, 2004, 14:15:01; Search time 24 Seconds (without alignments) 452.902 Million cell updates/sec 283366 seqs, 96191526 residues US-09-441-242A-2 612 AECPTLGEAVTDHPDRLWAW.....VYHIKIDGVEDMLLELLPDD 113 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Database

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

QY 61 MTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD	1 ABCPTLGEAVTDHPDRLWAWEKFVYLDEKQHAWLPLTIBIKDRLQLRVLLF 	Query Match 100.0%; Score 612; DB 2; Length 114; Best Local Similarity 100.0%; Pred. No. 1e-59; Matches 113; Conservative 0; Mismatches 0; Indels 0;	C;Genetics: A;Gene: GDB:TCL1 A;Cross-references: GDB:250785 A;Map position: 14q32.1-14q32.1	A;Accession: 138286 A;Molecule type: mRNA A;Residues: 1-114 <res> A;Cross-references: EMBL:X82240; NID:g624960; PIDN:CAA57708.1; PID:g624961</res>	A, Filtle: Identification of the TCL1 gene involved in T-cell malignancies. A, Factor number: I38286; MUID:95107991; PMID:7809072	C;Acce: V3-mar-1230 #sequence_revision v3-mar-1230 #sexc_change V3-mV7-1233 C;Accession [138286, SS1138] C;Accession [138286, SS1138] R;Virgilio, L.; Narducci, M.G.; 13056, M.; Ri	RESULT 1  I 38286  T cell leukemia/lymphoma protein TCL1 - human T cell leukemia-related protein TCL1 N;Alternate names: T-cell leukemia-related protein TCL1 C.Species: Homo sapiens (man) C.Steches: Homo sapiens (man)
114	60	Gaps 0;		g624961	ncies.	I.D.; Croce, C.M.; R	

C;Accession: S78532

R;Stern, M.H.; Soulier, J.; Rosenzwajg, M.; Nakahara, K.; Canki-Klain, N.; Aurias, A.; Oncogene 8, 2475-2483, 1993

A;Title: MTCP-1: a novel gene on the human chromosome Xq28 translocated to the T cell 1 \$78532 MTCP-1 protein splice form B1 - human C;Species: Homo sapiens (man) C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000 A;Title: MTCP-1: a novel gene on the human chromosome Xq28 translocated to the T cell 1 A;Reference number: I38045; MUID:93368950; PMID:8361760

A; Accession: S78532

A;Cross-references: EMBL: 224459; NID: g2252491; PIDN: CAA80828.1; PID: g2252492 A; Molecule type: DNA A; Residues: 1-107 < STE>

A;Gene: MTCP-1

C;Genetics:

A;Introne: 35/3; 92/3 C;Keywords: alternative splicing; T-cell proliferation

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A; Notatus. From A
A; Molecule type: DNA
A; Residues: 1-619 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB37296.1; PID:g13363345; GSPDB:GN00154
A; Cross-references: GB:BA000007; PIDN:BAB37296.1; PID:g13963345; GSPDB:GN00154
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AC0884
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                     glutathionylspermidine synthetase/amidase [imported] - Escherichia coli (strain O157:H7 C;Species: Escherichia coli (C;Pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0884
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A; Residues: 1-618 < PAR>
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  S
                                                                                                                                                                                                                                                                                                                                              R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
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16 RLWAWE----KFVYLDEKQHAWLPL-TIEIKDRLQLRVLLRREDVVLGRPM-TPTQIGPS
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29.7%;
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28.4%;
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Pred. No. 5.3e-17;
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H.
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e, N.; Farrar
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A85958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005174; NID:g12517552; PIDN:AAG58125.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:
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                                                                                                                                             A;Residues: 1-619 <BLAT>
A;Cross-references: GB:AE000381; GB:U00096; NID:g2367181;
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                    Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bollinger Jr., J.M.; Kwon, D.S.; Huisman, G.W.; Kolter, R.; Walsh, C.T. J. Biol. Chem. 270, 14031-14041, 1995
A;Title: Glutathionylspermidine metabolism in Escherichia coli. Purification, cloning, c A;Reference number: A57538; MUID:95294007; PMID:7775463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A85958
                                                                                                                                                                                                                                    A; Status: preliminary; nucleic
                                                                               ;Gene: gsp
;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A85958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
         Query Match
Best Local Similarity
                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.; Grotbeck, B.J.; Davis, N.W.; Lim, 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POCST
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                                                                               multifunctional enzyme
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         13.6%;
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Pred. No. 0.55
21; Mismatches
         Score
Pred.
                                                                                                                                                                                                                                      sequence
         83;
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DB
1.55;
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                                                                                                                                                                                                                                         shown; translation
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                               Length 619;
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                                                                                                                                                                        PIDN: AAC76024.1;
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                                                                                                                                                                                                                                           not
                                                                                                                                                                                                                                                                                                                                                                               V.; Riley, M.;
                                                                                                                                                                                                                                           shown
                                                                                                                                                                        PID:g1789361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O157:H7,
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